```
GenCore version 6.2.1
                 Copyright (c) 1993 - 2007 Biocceleration Ltd.
OM protein - protein search, using sw model
Run on:
               October 20, 2007, 03:44:28 ; Search time 100 Seconds
                                           (without alignments)
                                          871.101 Million cell updates/sec
Title:
               US-10-576-982-2
Perfect score: 438
               1 SYTSNASGSEAAAKAWIAGR......ASRYGSWTAAQQFWQANGWY 81
Sequence:
Scoring table: BLOSUM62
               Gapop 10.0 , Gapext 0.5
               3281787 segs, 1072124677 residues
Searched:
RESULT 2
Q8G8U9_9LACO
    Q8G8U9_9LACO PRELIMINARY; PRT; 289 AA.
    08G8U9;
AC
DT
    01-MAR-2003, integrated into UniProtKB/TrEMBL.
    01-MAR-2003, sequence version 1.
07-FEB-2006, entry version 7.
DT
DT
DE
    Aggregation promoting factor.
    Name=apf1; Synonyms=apf2;
GN
OS
    Lactobacillus gasseri.
OC
    Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
OC
    Lactobacillus.
\circ x
    NCBI_TaxID=1596;
RN
    [1]
    NUCLEOTIDE SEQUENCE.
RP
    STRAIN=ATCC 19992;
RC
RX
    MEDLINE=22338280; PubMed=12450842;
    DOI=10.1128/AEM.68.12.6172-6181.2002;
RX
    Ventura M., Jankovic I., Walker D.C., Pridmore R.D., Zink R.;
RT
    "Identification and characterization of novel surface proteins in
RT
    Lactobacillus johnsonii and Lactobacillus gasseri.";
RL
    Appl. Environ. Microbiol. 68:6172-6181(2002).
CC
CC
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CC
DR
    EMBL; AF543458; AAN64911.1; -; Genomic_DNA.
DR
    EMBL; AF543459; AAN64912.1; -; Genomic_DNA.
SQ.
    SEQUENCE 289 AA; 31297 MW; 59807D24B026DFEF CRC64;
 Query Match 88.8%; Score 389; DB 2; Length 289; Best Local Similarity 87.7%; Pred. No. 7.6e-32;
 Matches 71; Conservative
                              4; Mismatches 6; Indels
                                                              0; Gaps 0;
            1 SYTSNASGSEAAAKAWIAGRESGGNYNATNGQYIGKYQLAASYLGGDYSPANQERVADQY 60
QУ
             209 SYTSNASGSEAAAKAWIAGRESGGSYSARNGQYIGKYQLSASYLGGDYSAANQERVADNY 268
Db
          61 VASRYGSWTAAQQFWQANGWY 81
Qу
              1 1111111 11:111 1111
Db
         269 VKSRYGSWTGAQKFWQTNGWY 289
```